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           Score 16; DB 4; Length 14148;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KLINGER, KATHERINE W.
APPLICANT: LANDES, GREGORY M.
APPLICANT: BANN, TIMOTHY D.
APPLICANT: GONNORS, TIMOTHY D.
APPLICANT: DAGKOWSKI, WILLIAM R.
APPLICANT: GENLINO, GREGORY
APPLICANT: GIAN, FENG
APPLICANT: OIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEGURENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,443B
FILING DATE: 12-OCT-1994
CLASSIFFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 22; Matches 16; Conservative 0; Mismatches
                                                                    Mismatches
                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08323443B Patent No. 5654170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-08-658-136-2/c
; Sequence 2, Application US/08658136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCRACTAINT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25.351
REFERENCE/DOCKET NUMBER: 25.351
TELEPHONE: (212) 527-7700
TELEFAX: (212) 537-537
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
LENGTH: 31571 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
                Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 31571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3273 CGCGGGCGGCATCGT 328B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COGANISM: Homo sapiens invasorates source:
CLONE: PKD1 GENOMIC
US-08-323-443B-1
                                                                                                                                                  224 CGGCGGCGCCATCGT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGGCGGCGGCATCGT 16
                                                                                                                   1 CGGCGGGGGCATCGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                             NAME/KEY: misc_feature
LOGATION: B363..11741
OTHER INFORMATION: /note- "N-linked glycosylation
OTHER INFORMATION: sites at following locations: 8471, 8663, 8732, 8843,
*PATURE:
NAME/KEY: misc_feature
LOCATON: 4574..814
OTHER INFORMATION: Anote- "N-linked glycosylation
OTHER INFORMATION: sites at following locations: 4559, 4574, 4631, 4763,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 212, 278
OTHER INFORMATION: /note- "Possible hinge sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 10178..10239
OTHER INFORMATION: \(\text{Ancte-}\) Predicted transmembrane
OTHER INFORMATION: \(\text{Accession}\)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATURE:
NAME/KEY: misc_feature
LOCATION: 10686..10946
OTHER INFORMATION: /note= "Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 7949.8009
OTHER INFORMATION: /note= "Predicted transmembrane
OTHER INFORMATION: dommain"
                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 8288.8348
OTHER INFORMATION: /note="Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 9434, 9494
OTHER INFORMATION: /note= "Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 10052.10112
OTHER INFORMATION: Cote- "Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 10955.11015
OTHER INFORMATION: Lote- "Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 11216.11276
OTHER INFORMATION: Lote-"Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 11894.11554
OTHER INFORMATION: Conte-"Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 12293.12353
OTHER INFORMATION: /Aote= 'Predicted transmembrane
OTHER INFORMATION: domain'
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LOCATION: 12377.12437
OTHER INFORMATION: /note="Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOCATION: 279
TOTHER INFORMATION: /note- "Cleavage site"
CS-09-032-469-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 279
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Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1115, Ap
Sequence 6, Appli
                                                                                                                     January 31, 2003, 18:57:08; Search time 18:3667 Seconds (without alignments) 317.252 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 595,
Sequence 66, A
Sequence 1, Ap
Sequence 8, Ap
Sequence 8, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: /cgn2_6/ptodate/2/ina/5h_COMB.seq:*
    /cgn2_6/ptodata/2/ina/5b_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6b_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/fullesl:seq:*
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                     441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                     US-09-904-968A-19
19
1 ggtcgcgctgtggcgaagg 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_NA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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53526
53577
633
3396
                                                                                                                                                                                                         Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                          Run on:
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us-09-904-968a-19.rni

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic
STRANDEDNESS:
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                                          ö
Length 53526;
                                                                                                                                                                                                                                                                                             APPLICANT: LANDES, GREGERY M
APPLICANT: DURN, TIMOTHY D
APPLICANT: DURNORS, TIMOTHY D
APPLICANT: DAKNOWSKI, WILLIAM
APPLICANT: GREMINO, GREGORY
APPLICANT: GLAM, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PACTEDIN PC-DOS/MS-DOS
SOFTMARE: PACTEDIN PC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 19; Best Local Similarity 100.0%; Pred. No. Matches 19; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : GENZYME CORPORATION ONE MOUNTAIN ROAD
                                                                                                                                                                                                      2, Application US/08658136
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                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLACE DATE: 435
CLASSIFICATION: 435
CLASSIFICATION: TRABETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGTCGCGCTGTGGCCAAGG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 53526 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                               1 GGTCGCGCTGTGGCGAAGG 19
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TITLE OF INVENTION: WILLIAD TITLE OF INVENTION: AND USES THEREOF CORRESPONDENCE ASHBYA GOSSYPII NUMBER OF SEQUENCES OF ASHBYA GOSSYPII NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 623264artis Cordoration: 3054 Cordwallian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 53577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
APPLICANT: GERMING, GREGORY
APPLICANT: GIRMLY, FENG
TITLE OF INVENTION: DELYCYSTIC KIDNEY DISEASE GENE
MUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
STREET: ONE MOUNTAIN ROAD
STREET: ONE MOUNTAIN ROAD
CITY: FRAINGRAM
STATE: MASSACHUSETTS
COUNTY: DAS COMPATER READABLE FORM:
MEDIUM TYPE: TIOPPY disk
COMPUTER: TAN FO COMPATION
COMPUTER: TAN FO COMPATION
FILLING PATENTING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: PACABLE
OPERATING SYSTEM: PC-LOS/MS-DOS
CURRENT APPLICATION DATA:
REPLIEGATION NUMBER: US/08/658,136
FILLING DATE:
CLASSIFICATION NUMBER: US/08/658,136
ATTORNET/AGENT INFORMATION:
NAME: LASSEN, BLIZABETH
REGISTRATION NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: No. 6339264artis Corporation
CITY: Research Triangle Park
STRATE: No. 6239264th Carolina
COUNTRY: USA
COMPRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DD 3334 GGTCGCGTGTGGCGAAGG 3352
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Sequence Sequence Sequence

ALIGNMENTS

Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence seguence

85-1998-41 28-155-16 28-155-17 39-3338-59 37-7388-59

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APPLICANT: KLINGE, KATHERINE W.
APPLICANT: KLINGE, KATHERINE W.
APPLICANT: LANDES, GREGORY W.
APPLICANT: BURN, TIMOTHY D.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: GENALNO, GREGORY
APPLICANT: GENALNO, GREGORY
APPLICANT: GLAN, FENALNO, GREGORY
APPLICANT: OLAN, FENALNO, GREGORY
APPLICANT: UNENALNO, GREGORY
GREGORY AND ANDRESSE: DATHY & DATHY & DATHY
GREGORY ANDRESSE: DATHY &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 10022
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TELOPPY disk
COMPUTER: TEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
SOFTWARE: PATENTION DATA:
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/323,443B
FILING DATE: 12-CGT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
MAME: LUMGHIG, S. PETEN
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0372/0A462
FELECOMONICATION NUMBER: 25,351
FELECOMONICATION NUMBER: 25,351
FELECOMONICATION NUMBER: 0372/0A462
FELECOMONICATION NUMBER: 25,351
FELECOMONICATION NUMBER: 35,351
FELECOMONICATION NUMBER: 35,37
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
TVPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                           5-08-887-798-23
5-08-990-823-19
5-09-280-116-258
5-08-796-792-3
                                       US-06-128-155-17
US-08-189-333F-59
US-08-149-103-1
US-08-149-103-1
US-08-994-489-1
US-08-994-689-1
US-08-994-638-2
US-08-994-638-2
US-08-994-638-3
US-08-994-638-3
US-08-894-638-3
US-08-894-638-3
US-08-894-638-3
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RYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANICE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 31571 base pairs
nucleic acid
EDNESS: single
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IMMEDIATE SOURCE:
CLONE: PKDI GENOMIC
                152331
176373
74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
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Sequence 102, App
Sequence 102, App
Sequence 101, App
Sequence 101, App
Sequence 101, App
Sequence 101, App
Sequence 102, App
Sequence 102, App
Sequence 102, App
Sequence 103, App
Sequence 104, App
Sequence 105, App
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Sequence 2, Appli
                                                                                                                                                               search time 25.1333 Seconds (without alignments) 317.252 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/ptotus_COMB.seq:*
/cgn2_6/ptodata/2/ina/ptotus_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                         US-09-904-968A-4
26
1 ccacctcatcgccccttcctaagcat 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441352 segs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                            January 31, 2003, 18:57:08
                                                                                                                                                                                                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_NA:
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Maximum DB seq length: 200000000
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Match ]
                                                                                                                                                                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
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DB 3; Length 53526;
    Length 31571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
OPERATING SYSTEM: PC-TOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/658,136
FILING DATE:
Query Match
Best Local Similarity 100.0%; Score 26; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATORNEY AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4315 CCACCTCATCGCCCTTCCTAAGCAT 4290
                                                                                           AFFLICATION: POLYCYSTIC KI
NUMBER OF SEQUENCES: 58
NORRESPONDENCE ADDRESS: A
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                      Sequence 2, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOMSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: GIAN, FENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: 11
; MOLECULE TYPE:
US-08-658-136-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -08-658-136-1/c
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Sequence 1, Application US/08658136 Patent No. 6071717

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TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
WITH REDUCED INHIBITION OF CELLULAR MACRO-MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: Seed Intellectual Property Law Group PLLC STREET: 701 Fifth Avenue, Suite 6300
LANT: CONNORS, TIMOTHY D
APLICANT: DACKOWSKI, WILLIAM
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SECURNCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSE: GENYTHEN CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: PRAMINGRAM
SITE: MASSACHUSETIS
COUNTRY: USA
ZIP: USA
ZIP: USA
MEDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 26; DB
; Pred. No. 0.0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dubensky Jr., Thomas W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCACCICATGGCCCCTICCIAAGCAT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-658-136-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 26; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,84
REFERENCE/DOCKET NUMBER: G
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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sequence 7, Appli
Sequence 12, Appli
Sequence 12, Appl
Sequence 51, Appl
Sequence 53, Appl
Sequence 168, Appl
Sequence 168, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 66, Appl
Sequenc
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LANDES, GREGORY M.
APPLICANT: BURN, THAOTHY C.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: GRENINO, GREGORY
APPLICANT: GRENINO, GREGORY
APPLICANT: GLAW, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:

WEDLUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SISTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTEN RC-BESS #1.0, Version #1.30
SOFTWARE: PALENTEN RDARA:
CURRENT APPLICATION DARA:
APPLICATION NUMBR: 12-CCT-1994
CLASSIFICATION: US/08/323,443B
FILING DATE: 12-CCT-1994
CLASSIFICATION: 25,351
ATTORNEY.AGENT INFORMATION:
NAME: Ludwig, S. Peter
RETERENCE/DOCKET NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 25,351
RETERENCE/COMPUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1:
SEGOURDE CHARACTERISTICS:
LENGTH: 31571 base pairs
TYPE: nucledc acid
STRANDEDRESS: $1641
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-176-657-4
US-09-643-597-358
US-09-643-597-168
US-09-193-5620-31
US-09-64-597-160
US-08-05-1388-15
US-08-976-259-64
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MOLECULE TYPE:, DNA (genomic)
HYPOTHEFICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: PKDİ GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NY
COUNTRY: USA
ZIP: 10022
                                                                                                                                                                                                                                                            January 31, 2003; 18:57:08; Search time 28:0333 Seconds (without alignments) 317.252 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3
Sequence 1
Sequence 3
Sequence 3
Sequence 1
Sequence 1
Sequence 1
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: /cgn2_6/ptodata/2/ina/5A_CCMB.seq:*
    /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
    /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
    /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
    /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*

                                          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                         US-09-904-968A-3
29
I ccatccacctgctgtgtgcctggtaaat 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table: IDENTITY_NUC Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                    Run on:
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TILLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE NUMBER OF SEQUENCES: 58
CORRESPONDENCES: 58
CORRESPONDENCE ADERES: ADDRESSE: GENEYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTR: USA
LIP: 01701
COMPUTER FRANABLE FORM:
MEDIUM TYPE: Floppy disk

ALELIA AC GREGORY FENG

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS, SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/658,136

APPLICALL...
APPLICALL...
FILING DATE.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: 31,845
TELECHOMINICATION INPORMATION:
TELEPHONE: 508-872-5415
TELEPHONE: 508-872-5415

SECUENCE CHARACT

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Gaps
     Length 31571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 53526;
                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 01701
ZIP: 01701
COMPUTER READALD FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
COMPUTER: 18M PC compatible
COMPUTER: PEC-TOS/MS-DOS
SOFTMARE: PETENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NAM:
RPPLICATION NOMBER: US/08/658,136
  DB 1:
Query Match
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                    APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY W
ARPLICANT: BURN, TIMOTHY C
APPLICANT: DACKOWSI, INCLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
TITLE OF INVENTION: POLYCYSTIC KIDNEY DIS
CORRESPONDENCES: 58
CORRESPONDENCES: 58
ADDRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.0%; Score 29; Best Local Similarity 100.0%; Pred. No. (Matches 29; Conservative 0; Mismatche
                                                                                                                          Db 1448 ccarccaccrdcrdrdrdrdrdrar 1476
                                                                                     1 CCATCCACCIGCIGTGTGACCIGGTAAAT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESS CARTAGE ENLYMENTED HOUNTAIN ROAD
                                                                                                                                                                                                                                      Sequence 2, Application US/08658136
Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genemic)
US-08-658-136-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
TORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MASSACHUSETTS
                                                                                     õ
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-479-309-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18.4; D
Pred. No. 38;
O; Mismatches
                                                                                                                                              GENERAL INFORMATION:
APPLICANT MENG, Macdong
APPLICANT DU, Chunying
TILLE OF INFURINION: Activators of Caspases;
TILE PEPERBUCE: UTSD630
CURRENT APPLICATION NUMBER: US/09/479,309
CURRENT APPLICATION NUMBER: 2000-01-06
SOFTWARE: PATENTION NOS: 6
SOFTWARE: PATENTION Ver. 2.1
SEQ ID NO 3: 6
LENGTH: 20
US-09-479-309-3/c
; Sequence 3, Application US/09479309
; Patent No. 6110691
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 78:6%;
Matches 22; Conservative
```

2043 CCATCCACCTGCTGTGACCTGGTAAAT 2071

Application US/08658136

KLINGER, KATHERINE W LANDES, GREGORY M BURN, TIMOTHY C

APPLICANT: APPLICANT: APPLICANT:

1 CCATCCACCTGCTGTGACCTGGTAAAT 29

ô

Length 53577;

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 29; Conservative 0; Mismatches

DNA (genomic)

, MOLECULE TYPE: US-08-658-136-1

Qy : 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29

Page 1

us-09-904-968a-3.rni

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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo saplens
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKD1 GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                           January 31, 2003, 18:57:08 : Search time 28.0333 Seconds (without alignments) 317.252 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17
Sequence 16
Sequence 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/lna/5A_COMB.seq:*
/cgn2_6/ptodata/2/lna/6A_COMB.seq:*
/cgn2_6/ptodata/2/lna/6A_COMB.seq:*
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/cgn2_6/ptodata/2/lna/pcTU2_COMB.seq:*
/cgn2_6/ptodata/2/lna/pcTU2_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-844-634-17
US-09-844-634-17
US-09-128-155-16
US-08-128-155-17
US-08-724-394A-21
US-08-724-394A-21
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                                                                                                                                                               US-09-904-968A-3
29
I ccatccacctgctgtgtgacctggtaaat 29
                                                                                                                                                                                                                                                                                                                otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-333-576C-3
US-08-289-222E-1
US-09-054-526B-1
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                                                                                                                                                                                                                                                                                   441362-seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                   Ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10,0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_NA:
                                                                                                                                                                                                                                                                                                                                                     linimum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
Query
Match Length DB
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1000.0 53526
1000.0 53526
63.4 720
63.4 9721
63.4 15621
63.4 156373
62.1 246240
62.1 246240
62.1 246240
62.1 246240
62.1 246240
62.1 246240
62.1 246240
                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                    coring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atabase :
                                                                                                                                                                                                                                                                                     earched:
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Sequence 7, April Sequence 18, April Sequence 124, April Sequence 51, April Sequence 4, April Sequence 4, April Sequence 158, April Sequence 158, April Sequence 168, 
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KINGER, KATHERINE W. APPLICANT: KINGER, KATHERINE W. APPLICANT: LANDES, GREGORY M. APPLICANT: LANDES, GREGORY M. APPLICANT: LANDES, GREGORY M. APPLICANT: CONNORS, TIMOTHY D. APPLICANT: CONNORS, TIMOTHY D. APPLICANT: GEMINO, GREGORY M. APPLICANT: GEMINO, GREGORY FENG TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE: NUMBER OF SEGURES: 8

APPLICANT: GLAN, FENG TIMOTHY PRODUCES: 8

CONRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: DAIDY & Daidy PC
STREET: NEW YOIK
STATE: NEW YOIK
STREET: BAN YOUR RELADED FORM: STREET: BAN YOUR RELADED FORM: CONPOTER: IBM PC COMPATIBLE OF STREET: PC-DOS/WS-DOS
COMPUTER: BAN PC COMPATIBLE OF STREET: PC-DOS/WS-DOS
COMPUTER: STATE: NOW YOIK
STREET: ADDRESSE: 12-OCT-1994
CLASSIFICATION NUMBER: US/08/32),443B
FILLING DATE: 12-OCT-1994
CLASSIFICATION NUMBER: US/08/32),443B
FILLING DATE: 12-OCT-1994
CLASSIFICATION NUMBER: US/08/32),443B
FILLING DATE: 12-OCT-1994
CLASSIFICATION NUMBER: US/08/32)
RECTERANTON NUMBER: US/08/32)
RECTERANTON FOR SEC ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
STRANDEDNESS: SINGLE
                             US-09-149-476-97

US-08-153-007-1

US-08-153-777-7

US-08-153-778-7

US-08-153-778-7

PCT-USS-206-73-7

US-08-912-1228-18

US-08-912-1228-51

US-08-912-1228-51

US-09-64-597-78-8

US-09-176-657-4

US-09-176-657-4

US-09-176-657-4

US-09-176-657-4

US-09-176-657-4

US-09-176-657-4

US-09-176-657-4

US-09-178-597-188

US-09-191-5627-31

US-08-191-5627-31

US-08-191-5627-31

US-08-191-5627-31

US-08-191-5627-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencentrated Action US/083234438
Fratentino (5) Frategraphy (1)
Sequentino (5) Frategraphy (1)
Sequent Information:
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equence 2, Application US/08658136 stent No. 6071717

us-09-904-968a-3.rni

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TYPE: DNA ATLIÉICIAl Sequence FEATURE: ORGANISM: PEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-479-309-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 53577:
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Best Local Similarity 78.6%; Pred. No. 38;
Matches 22; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
APPLICANT: CORNUL, WILLIAM APPLICANT: DACKOMSKI, WILLIAM APPLICANT: DACKOMSKI, GREGORY APPLICANT: GERLINO, GREGORY APPLICANT: GERLINO, ERGORY TILE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE TUMBER OF SEDUENCES: 58 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: GENUNTAIN ROAD APPREST: ONE WOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Xiaodong
APPLICANT: Wang, Xiaodong
APPLICANT: Word, Xiaodong
TILLE OF INVENTION: Activators of Caspases
FILE REPERENCE: USD0630
CURRENT APPLICATION NUMBER: US/09/479,309
CURRENT FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2 1
SEQ ID NO 3
LENGTH: 720
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US-09-479-309-3/c
: Sequence 3. Application US/09479309
: Patent No. 6110691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATONEY/AGENT INCORMATION:
NAME: LASSEN, ELIGABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEM,
TELECOMMUNICATION INVORMATION:
TELEFOME: 508-872-5415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTROL OF CONTROL CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 5357 base pairs TYPE: mucleic acid STRANDEDMESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
21P: 01701
                                                                                                                                                                           ö
                                                                                                                                                                                Gaps
                                                                             Ouery Match 100.04; Score 29; DB 1; Length 31571; Best Local Similarity 100.04; Pred. No. 0.002; Matches 29; Conservative 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: CANDRY TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: GERHING, GREGORY
APPLICANT: GERHING, GREGORY
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
```

COMPUTER READLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.25

CORRESPONDENCE ADDRAGG STORY ADDRESSEE: CONTRACTORY STREET: ONE HOUNTAIN ROAD

CITY: PRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA

SOFTWARE: Patentin Release #1.0, 1 CURRENT APPLICATION DATA: RPPLICATION WUMBER: US/08/658,136 FILING DATE:

CLASSIFICATION: 435
ATTORNEY/ARGNI INFORMATION:
NAME: LASSEN, ELLIABETH
REGISTRATION NUMBER: 31,845
REPERENCE/COCKTV NUMBER: GEN4-17.8
TELEPHONE: 508-872-8400
TELEFAX: 508-872-8415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

Ouery Match
100.0%; Score 29; DE
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 29; Conservative 0; Mismatches

TOPOLOGY: 11near MOLECULE TYPE: DNA (genomic) S-08-658-136-2

. 53526 base pairs nucleic acid

2043 CCATCCACCTGTGTGACCTGGTAAAT 2071

Sequence 1, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY W
APPLICANT: BURN, TIMOTHY C

Sequence 1, N. Sequence 5, A. Sequence 3, A. Sequence 3, A. Sequence 23, Sequence 23, Sequence 258, Sequence 3, A.
Sequence Seq

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APPLICANT: KLINGER, KATHERINE W.
APPLICANT: LANDES, GRECORY W.
APPLICANT: LANDES, GRECORY W.
APPLICANT: BURN, TIMOTHY C.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: DACKOMSKI, WILLIAM R.
APPLICANT: GEMINO, GREGORY
APPLICANT: GINN, FENG
TITLE OF INVENTION: POLYCYSTIC KINNEY DISHASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
Andressed
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REDIUM TYPE: RIOPPY disk
COMPUTER: EBM PC COMPALLDIE
COMPUTER: EBM PC COMPALLDIE
COMPUTER: EBM PC COMPALLDIE
COMPUTER: EBM PC COMPALLDIE
SOFTWARE: PACENTION DATA:
CURRENT APPLICATION DATA:
FILLICA DATE: 12-CC-194
CLASSIFICATION: 435
ATTORNEY/AREIT INFORMATION:
NAME: LUGAGE, S. PETEL
REFERENCE/DOCKET NUMBER: 25,351
REFERENCE/CATION INFORMATION:
TELEPHONE: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1:
FENDING READ IN NO: 1:
FENDING READ IN NO: 1:
FENDING READ IN NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psequence 1, Application US/08323443B
patent No. 5654170
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STREET: 805 Third Avenue
CIIY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                               January 31, 2003, 18:57:08 : Search time 25.1333 Seconds (without alignments) 317.252 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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2: /cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptcdata/2/ina/ptcV15_COMB.seq:*
6: /cgn2_6/ptcdata/2/ina/packfiles1.seq:*
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-904-968A-4
26
1 ccacctcatcgcccttcctaagcat 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441362 segs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                        OM nucleic - nucleic search, using sw model
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US-08-94
US-08-94
US-09-41
US-09-41
US-09-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                              Run on:
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ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION UNDHER: 31,045
REFERENCE/DOCKET UNHER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dubensky Jr., Thomas W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4314 CCACCTCATCGCCCTTCCTAAGCAT 4289
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Patent No. 6391632
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCACCTCATCGCCCCTTCCTAAGCAT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATID
OPERATING SYSTEM: PC-DOS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear : MOLECULE TYPE: DNA (genomic) US-08-658-136-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 53577 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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Duery Match
100.0%; Score 26; DB 1; Length 31571;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 26; Conservative 0; Mismatches 0; Indels 0
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0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALISH
OPERATING SYSTEM: PC-DOS/MS-DOS .
SOFTWARE: PATEMENT RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
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Best Local Similarity 100.0%; Pred. No. (
Matches 26; Conservative 0; Mismatche
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3-08-658-136-1/C

Sequence 1, Application US/08658136

Patent No. 6071717

GENERAL INFORMATION:
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NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/POCKET NUMBER: GEN4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-672-8400
                                                                                                                                                                                                                                                                                                                                                                            -08-658-136-2/c
Sequence 2, Application US/U3658136
Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOLECULE TYPE: DNA (genomic): 08-658-136-2
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STRANDEDNESS

APPLICANT: APPLICANT: APPLICANT:

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APPLICANT: DUDELLAY V...
POLO, JOHN M.
Belli, Barbara A.
Schleainger, Sondra
Dryga, Sergey A.
Frolow, Ilya
TILE OF INVENTION: RECOMBINANT ALPHAVIRUS-BASED VECTORS
WITH REDUCED INHIBITION OF CELLULAR MACRO-NOLECHLARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed Intellectual Property Law Group PLUC
STREET: 701 Fifth Avenue. Suite 6300
STATE: Washington
COUNTRY: USA
ZATE: Washington
COUNTRY: USA
ZIP: 98104-7792
COMPUTER READABLE FORM:
MEDIUM ITPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 53577; 0.004;
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GERGORY
APPLICANT: GERMINO, GERGORY
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCES: ABORESS:
ADDRESSEE: GENTWE CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRANCHARA
STRIE: WASSACHUSETTS
COUNTRY: USA
ZIP: OIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Thepy disk
COMPUTER: THE MP COMPATION OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Vorsion #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C8/658,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match.

100.0%; Score 26; Di
Best Local Similarity 100.0%; Pred. No. 0.(
Matches 26; Conservative 0; Mismatches
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us-09-904-968a-19.rni

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4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-323-443B-1/c
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US-08-323-443B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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115, Ap
                                                                                                                                                                                    January 31, 2003, 18:57:08; Search time 18.3667 Seconds (without alignments) 317.252 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1.
Sequence 6.5
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Sequence 8.5
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Sequence 3.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.3
Copyright (c) 1993 · 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441362 seqs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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I ggtcgcgcgtgggcgaagg 19
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Match
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Sequence 1,
Patent No. 516
Sequence 111,
Sequence 46,
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Sequence 1
Sequence 1
Sequence 5
Sequence 5
Sequence 2
Sequence 2
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APPLICANT: KLINGER, KATHERINE W.
APPLICANT: LANDES, GREGORY M.
APPLICANT: GUNN, TIMOHY C.
APPLICANT: GENERAL WILLIAM R.
APPLICANT: GENERAL WILLIAM R.
APPLICANT: GENERAL POLYCYSTIC KIDNEY DISFASE GENERAL OF INVERTOR: POLYCYSTIC KIDNEY DISFASE GENERAL WOMBER OF SEDURENES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: New YORK
COTTY: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,443B
FILING DATE: 12-CGT-1994
CLASSIFFCATION: 435
ATTONEY/AGENT INVORMATION:
MAME: LUMW49, S. PECET:
REGISTARTION NUMBER: 25,351
REGISTARTION NUMBER: 25,351
REGISTARTION NUMBER: 25,357
TELEPHONE: (212) 753-7700
TELEPHONE: (212) 753-6237
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 5168049-1
4 US-09-199-637A-111
3 US-08-822-586-46
4 US-09-103-840A-2
                                                          ALIGNMENTS
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
74.7 20235 1
74.7 20235 3
74.7 20235 3
74.7 32207 4
74.7 169998 4
73.7 23673 4
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73.6 9759 1
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us-09-904-968a-19.rni

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COMPUTER READABLE FORM:
MEDIUM TIPE: Floppy disk
COMPUTER:
COMPUTE
                                                                                              APPLICANT: OIAN FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
STREET: ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 100.0%; Score 19; Best Local Similarity 100.0%; Pred. No. Matches 19; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . JUMOLOGY: linear
HOLECULE TYPE: DNA (genomic)
US-08-658-136-1
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                                                                                                                                                                                                                                                                                                                    STREET: ONE MOUNTAIN R
CITY: FRANTINGRAM
STATE: MASSACHGEFTS
COUNTRY: USA
ZIP: 01701
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Overy Match 100.0%; Score 19; DB 1; Length 31571; BBSE Local Similarity 100.0%; Pred. No. 0.7? Matches 19; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDER, GREGORY M
APPLICANT: LANDER, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: BURN, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMING, GREGORY
APPLICANT: GINNEW, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
WUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
ODFRATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFTCATION: 435
ATTORNEY AGENT INCOMMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/COCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INCOMMATION:
TELECHOME: 508.872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2. Application US/08658136
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        1 GOTCGCGCTGTGGCGAAGG 19

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        12599 GGTCGCGCTGTGGCGAAGG 3581

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: MOLECULE TYPE: DNA (genomic)
US-08-658-136-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 3334 GGTCGCCTGTGCCGAAGC 3352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADVANCE ONE NO...
STREET. ONE NO...
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
...NTPY: USA
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SEQUENCES OF ASBBYA COSSYPTI
                                                                                                                                                                                                                                                                                                                                                                                                       5: No. 6239264artis Corporation 3054 Cornwallis Road
                                                                                    APPLICANT: Philippsen, Peter APPLICANT: Pohlwann, Rainer APPLICANT: Steiner, Sabine APPLICANT: Mohr, Christlee APPLICANT: Mohr, Christlee APPLICANT: Weedland, Jurgen APPLICANT: Rechischung, Corinne APPLICANT: Rebischung, Corinne APPLICANT: Rebischung, Corinne TITLE OF INVENTION: GENONIC DNA SEQUENTILE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
. Sequence 1115, Application US/08998416; Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: No. 6239264artis C. STRET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
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1, Application US/08658136

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Score 16; DB 4; Length 14148; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BURN, TIMOTHY C.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
TITLE OF INVENTION: POLYCYSTIC KICNEY DISEASE GENE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: LUGATG, S. PETER
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0372/0A462
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Vo
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,4438
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                            RESULT 5
US-08-658-136-2/c
: Sequence 2, Application US/08658135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: 'New York
STATE: NY
Query Match
Best Local Similarity 100.0%;
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 16; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 31571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 3273 CGCCGCCCCATCGT 3288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
INMEDIATE SOURCE:
CLONE: PKD1 GENOMIC '
                                                                                                                             224 CGGCGGCGCCATCGT 209
                                                                                                  1 CGCCGGCGGCATCGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; CLONE: F
US-08-323-443B-]
                                                                                            NAME/KEY: misc_feature
LOCATION: 9353.1174
OTHER INFORMATION: Anote- "N-linked glycosylation
OTHER INFORMATION: sites at following locations: 8471, 8663, 8732, 8843,
                     OTHER INFORMATION: /note= "N-linked glycosylation
OTHER INFORMATION: sites at following locations: 4559, 4574, 4631, 4763,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/RET: misc_feature
NAME/RET: 212.278
COTHER INFORMATION: /note- 'Possible hinge sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 11216.11276
OTHER INFORMATION: /note- "Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 12293..12353
OTHER INFORMATION: /note= "Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 12277-12437
OTHER INFORMATION: /note-"Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                         NAME/KEI: misc_feature
LOCATION: 7949. 18009
OTHER INFORMATION: /note- "Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 10052..10112
OTHER INFORMATION: /note- "Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 10178..10238
OTHER INFORMATION: /note- "Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 10955..11015
OTHER INFORMATION: Acote= "Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 8288.8348
OTHER INFORMATION: /note= "Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 9434.
OTHER INFORMATION: /note= "Predicted transmembrane
OTHER INFORMATION: domain".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 10886..10946
OTHER INFORMATION: /note= "Predicted transmembrane
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 11894.11954
OTHER INFORMATION: /note= Predicted transmembrane
OTHER INFORMATION: domain*
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